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(REV. 2-82) Patent and Trademark OfficeAtty. Docket No.
A31869-A 070050.1046Serial No.
09/549,827**INFORMATION DISCLOSURE STATEMENT
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Andrey Rzhetsky et al.Filing Date
April 14, 2000Group
1631**U.S. PATENT DOCUMENTS**

*Exam. Init.	Document No.	Date	Name	Class	Subclass	Filing Date if Appropriate

FOREIGN PATENT DOCUMENT

Document No.	Date	Country	Class	SubClass	Translator Yes No

OTHER DOCUMENTS (including Author, Title Date, Pertinent Pages, Etc.)

<i>A</i>		Ballinger CA et al., 1999, "Identification of CHIP, a novel tetratricopeptide repeat-containing protein that interacts with heat shock proteins and negatively regulates chaperone functions," <i>Mol Cell. Biol.</i> 19:4535-4545.
<i>A</i>		Barabasi and Albert, 1999, "Emergence of scaling in random networks," <i>Science</i> 286:509-512.
<i>A</i>		Enright AJ et al., 1999, "Protein interaction maps for complete genomes based on gene fusion events," <i>Nature</i> 402:86-90.
<i>A</i>		Marcotte EM et al., 1999, "Detecting protein function and protein-protein interactions from genome sequences," <i>Science</i> 285:751-753.
<i>A</i>		Ruecknagel KP et al., 1999, Dihydrolipoamide S-Succinyltransferase Precursor, Accession XUBYSD (gi 2144399)

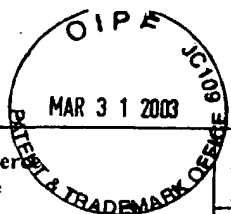
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<i>A</i>		Bailey et al., 1998, "Analysis of EST-driven gene annotation in human genomic sequence," <i>Genome Research</i> 8:362-376.
		Bono et al., 1998, "Reconstruction of amino acid biosynthesis pathways from the complete genome sequence," <i>Genome Res.</i> 8:203-210.
		Friedman C et al., 1998, "Evaluating natural language processing," <i>Methods of Information in Medicine</i> 37:334-44.
		Goto S et al., 1998, "LIGAND:chemical database for enzymes reactions," <i>Nucleic Acid Research</i> 14:591-599.
		Grundy, 1998, "Homology detection via family pairwise search," <i>J. Computational Biology</i> 5:479-491.
		Hu et al., 1998, "WD-40 repeat region regulates Apaf-1 self-association and procaspase-9 activation," <i>J. Biol. Chem.</i> 273:33489-33494.
		Sonnhammer ELL et al., 1998, "Pfam:multiple sequence alignments and HMM profiles of protein domains," <i>Nucleic Acids Research</i> 26(1):320-322.
		Wu SK et al., 1998, "Molecular role for the Rab binding platform of guanine nucleotide dissociation inhibitor in endoplasmic reticulum to golgi transport," <i>J. Biol. Chem.</i> 273:26931-26938.
		Yuan et al., 1998, "Towards detection of orthologues in sequence databases," <i>Bioinformatics</i> 14:285-289.
		Altschul et al., 1997, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," <i>Nucleic Acids Research</i> 25:3389-3402.
		Attwood TK et al., 1997, "The PRINTS database of protein fingerprints:a novel information resource for computational molecular biology," <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.
<i>A</i>		Cserzo M et al., 1997, "Prediction of transmembrane α -helices in prokaryotic membrane proteins:the dense alignment surface method," <i>Protein Engineering</i> 10:673-676.
<i>A</i>		Goto et al., 1997, "Organizing and computing metabolic pathway data in terms of binary relations," <i>Pac. Symp. Biocomput.</i> 2:175-186.

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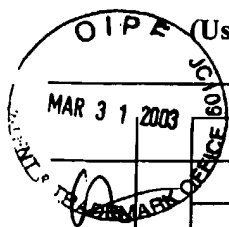
INFORMATION DISCLOSURE STATEMENT BY APPLICANT

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Applicant
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Group
1631



Grundy et al., 1997, "Hidden Markov model analysis of motifs in steroid dehydrogenases and their homologs," *Biochem Biophys. Res. Commun.* **231**(3):760-766.

Grundy WN et al., 1997, "Meta-MEME: motif-based hidden Markov models of protein families," *CABIOS* **13**:397-406.

Mushegian AR et al., 1997, "Positionally cloned human disease genes: patterns of evolutionary conservation and functional motifs," *Proc. Natl. Acad. Sci. USA* **94**:5831-5836.

Neuwald, 1997, "Extracting protein alignment models from the sequence database," *Nucleic Acids Research* **25**:1665-1677.

Pearson, 1997, "Identifying distantly related protein sequences," *CABIOS*, **13**:325-332;

Pena et al., 1997, "Stress-induced apoptosis and the sphingomyelin pathway," *Biochem Pharmacol.*, **53**:615-621.

Rogers MA et al., 1997, "Sequences and differential expression of the three novel human type II hair keratins," *Differentiation* **61**:187-194.

Selkov, E et al., 1997, "The metabolic pathway collection: an update," *Nucleic Acids Research* **25**:37-38.

Sharkey et al., 1997, "Hox genes in evolution: protein surfaces and paralog groups," *TIG* **13**:145-151.

Skvorak AB et al., 1997, "An ancient conserved gene expressed in the human inner ear: identification, expression analysis, and chromosome mapping of human and mouse antequitin (ATQ1), *Genomics* **46**:191-199.

Sonnhammer ELL et al., 1997, Pfam: A comprehensive database of protein domains families based on seed alignments, *Proteins Structure Function and Genetics* **28**:405-420.

NY02:433911.1

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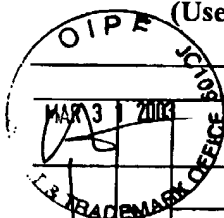
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Group
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Tatusov RL et al., 1997, "A genomic perspective on protein families," *Science* 278:631-637.

Boskovic J et al., 1996, Transcription Factor GRF10, Accession A25872 (gi|82888).

Bucher et al., 1996, "A flexible motif search technique based on generalized profiles," *Comput. Chem.*, 20:3-23.

Felsenstein J, 1996, "Inferring phylogenies from protein sequence by parsimony, distance, and likelihood means," *Methods in Enzymology* 266:418-427.

Gilks WR et al., eds., 1996, *Markov Chain Monte Carlo Practice*, Chapman & Hall/CRC, New York.

Gustafsson C et al., 1996, "Identification of new RNA modifying enzymes by iterative genome search using known modifying enzymes as probes," *Nucleic Acids Research* 24:3756-3762.

Jain NL et al., 1996, "Identification of suspected tuberculosis patients based on natural language processing of chest radiograph reports," *Proc. AMIA Annu Fall Symp* 542-546.

James CM et al., 1996, Cell Division Control Protein CDC43, Accession RGBY43 (gi|2144611).

Koonin EV et al., 1996, "Protein sequence comparison at sequence scale," *Methods in Enzymology* 266:295-323.

Mathews S et al., 1996, "The phytochrome family in grasses (Poaceae): A phlogeny and evidence that grasses have a subset of the loci found in dicot angiosperms," *Mol. Biol. Evol.*, 13:1141-1150

Miklos GLG, et al., 1996, "The role of the genome project in determining gene function: insights from model organisms," *Cell* 86:521-529.

Selkov et al., 1996, "The metabolic pathway collection from EMP: the enzymes and metabolic pathways database," *Nucleic Acids Research* 24:26-28.

Wu CH et al., 1996, "Motif identification neural design for rapid and sensitive protein family search," *Comput. Appl. Biosci* 12:109-118.

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Group
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Bailey et al. 1995, "The value of prior knowledge in discovering motifs," *Proc. Int Conf Intell Sys Biol.* 3:21-29.

Boldin et al., 1995, "A novel protein that interacts with the death domain of Fas./APO1 contains a sequence motif related to the death domain," *J Biol Chem*, 270:7795-8.

Friedman et al., 1995, "Natural language processing in an operational clinical information system," *Natural Language Engineering*, 1:83-108.

Green PJ, 1995, "Reversible Markov chain Monte Carlo computation and Bayesian model determination," *Biometrika* 82:711-732.

Hofmann et al., 1995, "The death domain motif found in Fas(Apo-1) and TNF receptor is present in proteins involved in apoptosis and axonal guidance," *FEBS Lett*, 371:321-3.

Hripcsak G et al., "Unlocking clinical data from narrative reports: a study of natural language processing," 1995, *Ann. Intern Med.* 122:681-688.

Hurlin PJ., 1995, "Mad3 and Mad4: novel Max-interacting transcriptional repressors that suppress c-myc dependent transformation and are expressed during neural and epidermal differentiation," *EMBO* 14:5646-59.

Neuwald AF et al., 1995, "Gibbs motif sampling: detection of bacterial outer membrane protein repeats," *Protein Sci.* 4:1618-1632.

Purnelle B et al., 1995, Pre-mRNA Splicing Factor PRP21, Accession S23553 (gi|280467)

Yang Z et al., 1995, "Maximum likelihood trees from DNA sequences: A peculiar statistical estimation problem," *Syst. Biol.* 44:384-399.

Zweigenbaum et al., 1995, "A multi-lingual architecture for building a normalised conceptual representation from medical language," *AMIA*, 357-361

NY02:433911.1

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Claverie, 1994, "Some useful statistical properties of position-weight matrices," *Comput. Chem.*, 18:287-94.

Churcher C, 1994, Dihydrolipoamide Dehydrogenase Precursor, Accession A30151 (gi|82983)

Contreras R et al., 1994, Hypothetical Protein YBL067C, Accession S45803 (gi|626480)

Entian KD et al., 1994, Omnipotent Suppressor Protein SUP45, Accession S46014 (gi|626763)

Gaillon L et al., 1994, Transcription Factor BAS1, Accession A40083 (gi|101447)

Hamlyn N et al., 1994, Oxoglutarate Dehydrogenase Precursor, Accession DEBY (gi|1070439)

Kazic 1994, "Representation of biochemistry for modeling organisms," In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494.

Kazic, 1994, "Biochemical databases: Challenges and opportunities," In: New Data Challenges in Our Information Age Glaesar, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140.

Krogh et al., 1994, "Hidden Markov Models in computational biology, applications to protein modeling," *J. Mol. Biol.* 235:1501-1531.

Lenert et al., 1994, "Automated linkage of free-text description of patients with a practice guideline," *AMIA*, 274-278.

Murphy L et al., 1994, Suppressor 2 Protein, Accession EFBY52 (gi|72877)

Rieger M, 1994, Protein Farnesyltransferase Chain RAM2, Accession P29703 (gi|266880)

Tatusov RL et al., 1994, "Detection of conserved segments in proteins: Iterative scanning of sequence databases with alignment blocks," *Proc. Natl Acad. Sci. USA* 91:12091-12095.

NY02:433911.1

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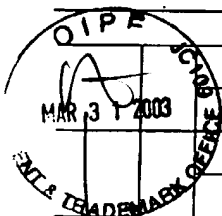
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Orengo et al., 1993, "A local alignment method for protein structure motifs," *J Mol Biol* 233(3):488-497.

Ullrich O et al., 1993, "Rab GDP dissociation inhibitor as a general regulator for the membrane association of Rab proteins," *J. Biol. Chem.* 268:18143-18150.

Venezia, 1993, "Rapid motif compliance scoring with match weight sets," *Comput Appl Biosci*, 9:65-9.

Baud et al., 1992, "Natural language processing and semantical representation of medical texts," *Meth. Info. Med.*, 31:117-125.

Peitgen HO, Juregens H, Saupe D, 1992, *Chaos and Fractals: New Frontiers of Science*, Springer Verlag, New York

Hirst et al., 1991, "Prediction of ATP-binding motifs: a comparison of a perceptron-type neural network and a consensus sequence method," *Prot Eng*, 4:615-623.

Altschul et al., 1990, "Basic local alignment search tool," *J. Mol. Biol.* 215:403-410.

Goldman N, 1990, "Maximum likelihood inference of phylogenetic trees, with special references to a poisson process model of DNA substitution and to parsimony analyses," *Syst. Zoo.* 39:345-361.

Haug et al., 1990, "Computerized extraction of coded findings from free-text radiologic reports," *Radiology*, 174:543-548.

Karlin S et al., 1990, "Methods for assessing the statistical significance of the molecular sequences features by using general scoring schemes," *Proc. Natl. Acad. Sci. USA* 87:2264-2268

Pamilo P et al., 1988, "Relationship between gene tree and species trees," *Mol. Biol. Evol.* 5:568-583.

Saitou N, 1987, "The neighbor-joining method: A new method for reconstructing phylogenetic trees," *Mol. Biol. Evol.* 4:406-425.

Fitch WM, 1974, "Evolutionary trees with minimum nucleotide replacements from amino acid sequences," *J. Mol. Evol.* 3:263-278.

NY02:433911.1

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Felsenstein J, 1978, "Cases in which parsimony or compatibility methods will be positively misleading," *Syst. Zool.*, 27:401-410.

Fitch WM, 1970, "Distinguishing homologous from analogous proteins," *Syst. Zool.*, 19:99-113.

Hastings, 1970, "Monte Carlo sampling methods using Markov chains and their applications," *Biometrika* 57:97-109.

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